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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Bednarik et al.

Attorney Docket No.: PF138P1C1

Application Serial No.: Unassigned

Art Unit: Unassigned

Filed: Herewith

Examiner: Unassigned

Title: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2

STATEMENT UNDER 37 C.F.R. § 1.821

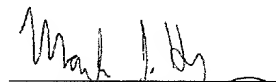
Commissioner for Patents
Washington, D.C. 20231

Sir:

Pursuant to 37 C.F.R. § 1.821(f), Applicants hereby certify that the sequence listing information recorded in computer readable form and submitted herewith is identical to the written (on paper) Sequence Listing submitted herewith.

Respectfully submitted,

Dated: July 12, 2001



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1

SEQUENCE LISTING

<110> Bednarik et al.

<120> Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2

<130> PF138P1C1

<150> US 08/461,031

<151> 1995-06-05

<150> PCT/US94/11914

<151> 1994-10-19

<160> 11

<170> PatentIn version 3.1

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<220>

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cctgcgttaa tccccctgat tccttgtggg ataaccgta ttccccct tagagtgaat 180

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cggcgcctc agaactagt gatcccccg gctccaggaa ttgccacga ccgggaggac 600

cgaggaggcg ccagactacg ggca atg gcg acc cgc agc cct ggc gtc gtg 652

Met Ala Thr Arg Ser Pro Gly Val Val
1 5

att atg gat gat tgg cca ggg tat gac ttg aat tta ttc acg tac cca 700

Ile Met Asp Asp Trp Pro Gly Tyr Asp Leu Asn Leu Phe Thr Tyr Pro
10 15 20 25

cag cac tat tat gga gac ttg gag tat gtc ctc atc cct cat ggt atc Gln His Tyr Tyr Gly Asp Leu Glu Tyr Val Leu Ile Pro His Gly Ile 30 35 40	748
att gtg gac aga att gag cgg ctg gcc aag gat att atg aaa gac ata Ile Val Asp Arg Ile Glu Arg Leu Ala Lys Asp Ile Met Lys Asp Ile 45 50 55	796
gga tat agt gac atc atg gtc ctg tgt gtg ctt aaa ggg ggg tac aaa Gly Tyr Ser Asp Ile Met Val Leu Cys Val Leu Lys Gly Gly Tyr Lys 60 65 70	844
ttc tgt gct gat ctc gta gaa cac ctt aag aac atc agc cga aat tca Phe Cys Ala Asp Leu Val Glu His Leu Lys Asn Ile Ser Arg Asn Ser 75 80 85	892
gat cgg ttt gtc tca atg aag gtt gat ttc atc aga cta aaa agt tac Asp Arg Phe Val Ser Met Lys Val Asp Phe Ile Arg Leu Lys Ser Tyr 90 95 100 105	940
agg aat gac cag tcc atg ggt gag atg cag ata atc gga ggc ggt gat Arg Asn Asp Gln Ser Met Gly Glu Met Gln Ile Ile Gly Gly Gly Asp 110 115 120	988
ctt tca acg ctg gct gga aag aat ttt ctc att gtt gag gat gtt gtc Leu Ser Thr Leu Ala Gly Lys Asn Phe Leu Ile Val Glu Asp Val Val 125 130 135	1036
gga act ggg agg acc atg aaa gca cta ctc agc aat ata gag aaa tac Gly Thr Gly Arg Thr Met Lys Ala Leu Leu Ser Asn Ile Glu Lys Tyr 140 145 150	1084
aag ccc aac atg att aag gta gcc agt ttg ttg gtg aag aga aca tcc Lys Pro Asn Met Ile Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser 155 160 165	1132
aga agt gac ggc ttt aga cct gac tat gct gga ttt gag att cca cac Arg Ser Asp Gly Phe Arg Pro Asp Tyr Ala Gly Phe Glu Ile Pro His 170 175 180 185	1180
tta ttt gtg gtg gga tat gcc tta gat tac aat gaa tac ttc aga gat Leu Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp 190 195 200	1228
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Tyr Asp Leu Asn Leu Phe Thr Tyr Pro Gln His Tyr Tyr Gly Asp Leu
 20 25 30

Glu Tyr Val Leu Ile Pro His Gly Ile Ile Val Asp Arg Ile Glu Arg
 35 40 45

Leu Ala Lys Asp Ile Met Lys Asp Ile Gly Tyr Ser Asp Ile Met Val
 50 55 60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Cys Ala Asp Leu Val Glu
 65 70 75 80

His Leu Lys Asn Ile Ser Arg Asn Ser Asp Arg Phe Val Ser Met Lys
 85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Arg Asn Asp Gln Ser Met Gly
 100 105 110

Glu Met Gln Ile Ile Gly Gly Gly Asp Leu Ser Thr Leu Ala Gly Lys
 115 120 125

Asn Phe Leu Ile Val Glu Asp Val Val Gly Thr Gly Arg Thr Met Lys
 130 135 140

Ala Leu Leu Ser Asn Ile Glu Lys Tyr Lys Pro Asn Met Ile Lys Val
 145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Asp Gly Phe Arg Pro
 165 170 175

Asp Tyr Ala Gly Phe Glu Ile Pro His Leu Phe Val Val Gly Tyr Ala
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Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile
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Asn Glu His Gly
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<213> Artificial Sequence

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<213> Homo sapiens

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20 25 30

Glu Arg Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
50 55 60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
65 70 75 80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
130 135 140

Thr Leu Leu Ser Leu Val Arg Gln Tyr Asn Pro Lys Met Val Lys Val
145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Pro Arg Ser Val Gly Tyr Lys Pro
165 170 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
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Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Val Cys Val Ile
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Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
210 215

<210> 8
<211> 218
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Table 1. Demographic characteristics of the study population	
Age (years)	65.5 ± 1.2
Gender (male/female)	10/10
Education (years)	12.5 ± 0.5
Occupation (white/blue)	10/10
Marital status (married/divorced/widowed)	10/10/0
Smoking status (smoker/non-smoker)	10/10
Alcohol consumption (yes/no)	10/10
Comorbidities (hypertension/diabetes/cholesterol)	10/10/10
Medication (antihypertensive/antidiabetic/anticholesterol)	10/10/10
Family history (hypertension/diabetes/cholesterol)	10/10/10
Physical activity (yes/no)	10/10
Stress level (low/moderate/high)	10/10/10
Sleep quality (good/poor)	10/10
Depression score (0-10)	2.5 ± 0.5
Overall health status (excellent/good/fair/poor)	10/10/10/10

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210 215 220

Lys Tyr Lys Ala Thr Ser Leu
225 230

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Glu Ala Glu Leu His Thr Arg Met Arg Gly Val Ala Gln Arg Ile Ala
20 25 30

Asp Asp Tyr Ser Asn Cys Asn Leu Lys Pro Leu Glu Asn Pro Leu Val
35 40 45

Ile Val Ser Val Leu Lys Gly Ser Phe Val Phe Thr Ala Asp Met Val
50 55 60

Arg Ile Leu Gly Asp Phe Gly Val Pro Thr Arg Val Glu Phe Leu Arg
65 70 75 80

Ala Ser Ser Tyr Gly His Asp Thr Lys Ser Cys Gly Arg Val Asp Val
85 90 95

Lys Ala Asp Gly Leu Cys Asp Ile Arg Gly Lys His Val Leu Val Leu
100 105 110

Glu Asp Ile Leu Asp Thr Ala Leu Thr Leu Arg Glu Val Val Asp Ser
115 120 125

Leu Lys Lys Ser Glu Pro Ala Ser Ile Lys Thr Leu Val Ala Ile Asp
130 135 140

Lys Pro Gly Gly Arg Lys Ile Pro Phe Thr Ala Glu Tyr Val Val Ala
145 150 155 160

Asp Val Pro Asn Val Phe Val Val Gly Tyr Gly Leu Asp Tyr Asp Gln
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Ser Tyr Arg Glu Val Arg Asp Val Val Ile Leu Lys Pro Ser Val Tyr
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Glu Thr Trp Gly Lys Glu Leu Glu Arg Arg Lys Ala Ala Gly Glu Ala
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Lys Arg
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